Ultrasound medical image deconvolution using CLEAN algorithm

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The reconstruction problem of ultrasound medical images using blind deconvolution algorithm has been recognized as one of the most important aspects in ultrasound images. The image resolution is deteriorated by many parameters such as noise or diffusive effects in tissues which produce the speckle noise. We intend to present the evaluation of the CLEAN algorithm, implemented in 1D for the ultrasound image deconvolution. This method supposes an iterative process for extracting the strongest point in a signal using a "dirty beam" which in our case is the estimated PSF. The PSF is extracted using the properties of the Homomorphic deconvolution and the Cepstrum properties with the outlier resistant de-noising algorithm. Our simulations are focused in two directions. Firstly, we want to verify how our method work with the reflectivity functions contaminated with different types of noise and secondly, we test its limits in function of the biological tissues scatters number.

1 Introduction

The medical diagnostic using ultrasounds has intensively used since the early 1980s, but scanner cost and spatial dimensions have limited its use to hospital utilisation for decades [1]. Nowadays, despite of the technological level, an ultrasound image with good resolution is difficult to obtain. The main problems (which cause a weak resolution) are the physics problem resulting from reflection, refraction and deflection of ultrasound waves from different kinds of tissues (with different acoustic impedance) and the convolution of the received signal with the transfer function of the acquisition system.

The problem of image deconvolution (or, equivalently, restoration or deblurring) naturally arises from this scenario. Its goal is the enhancement of image resolution and contrast by the restoration of an estimate of the true image. Image restoration is a very common problem in image processing, encountered in a wide variety of technical areas as astronomy, seismology, microscopy and medical imaging.

In literature, two main approaches are most common when dealing with image deconvolution. The first incorporates the Point Spread Function (PSF) estimation procedure within the deconvolution algorithm. In the second approach, PSF and true image estimation are two disjoint tasks. Within this approach, these procedures can be implemented by relatively simple algorithms, possibly suitable for real-time implementation. The most important algorithm utilised in the PSF estimation are combined cepstrum and homomorphic deconvolution properties. First, the method was introduced in ultrasound domain in [2]. The estimated PSF was calculated from the radio-frequency (RF) signal in 1D dimension. This method has been extended for 2D dimensions (using booth the RF signals or their envelope) and 3D (with RF signals.) [3, 4]. The homomorphic deconvolution was improved using a series of improvements like outliers resistant denoising for a better reflectivity function and noise suppression or phase recovery algorithms [5, 6]. All these method were tested in some deconvolution methods like, Wiener filter or inverse filter with some regularisation methods. An interesting approach was proposed also, starting from the initial PSF estimate, a new regularised inverse filter is estimated using the assumption of band limited spectrum for and the b-splines properties [7].

The CLEAN deconvolution was proposed in radio astronomy by Hogbom in 1974 [8]. The technique is used for suppressing the lateral side lobes of the acquisition system of the celestial images. Outside astronomy, CLEAN is applied to a huge application range. The simplicity of the algorithm (and of its implementation) and the excellent results have encouraged experimentation and adoption in other fields [9]. See, for example: optical coherence imaging of living tissue - magnetic resonance [10], synthesis aperture AR sonar imaging [11], characterisation of multiple input-multiple output(MIMO) systems [12], coherent and incoherent microwave imaging [13, 14, 15], data compression [16] and rinding subsurface objects using seismic waves [17]. In the ultrasound medical images this algorithm is almost missing. However, the most important work was proposed in [18]. They propose an iterative deconvolution, inspired by CLEAN algorithm, designed to deal with both non-minimum phase transducer impulse responses and scattering events not aligned with the sampling grid. Also, s study was proposed using a combination of the CLEAN algorithm and constant false alarm rate (CFAR) processing, developed for use in radar systems [19].

In this paper, we proposed a blind time domain deconvolution, using the CLEAN algorithm to extract the tissues reflectivity function from the measured RF signals. Indeed, CLEAN was able to extract the peaks from a blurred signal using an specific PSF. Moreover, CLEAN is a method easy to implement: its main mathematical operation is the subtraction, easy to execute with low computation power systems. The purpose of our study, led by the blind aspect and the novelty, was to make a quantitative evaluation of its performances, *i.e.* how much among the input reflectivity function signal peaks is recovered and what are the constraints and limitations. Moreover, once the CLEAN properties to offer different results in function of the selected exit threshold, we wanted to test the implication of its value.

The paper is organized as follows: Section 2 presents method utilised for algorithm implementation; in Section 3 we present the experiments description and motivation, Section 4 presents the experiment and results and, in Section 5 conclusions are presented.

2 Methods description

In this paper, we intended to present a new technique based on homomorphic deconvolution and CLEAN algorithm starting from the RF signal envelope. The simulations were realised for the RF signal whose reflectivity function is supposed to have a non Gaussian distribution. The tissue was usually composed of diffusive scatterers, superimposed with a sparse structure of a number of specular reflectors. The problem was divided in two steps: estimation of the PSF firstly and, deconvolution secondly using the estimated PSF to obtain the reflectivity function of the scanned tissues.

The main idea in the ultrasound pulse estimation was that it was a smooth function and the sparse reflectivity function had a wide and more uniform spectrum. Using this assumption one can change the signals separation problems in a denoising method. For this we used the cepstrum and homo-

morphic deconvolution properties. In a general case, the received signal was the result of the convolution between the pulse of the ultrasound scanner and the tissue reflectivity:

$$y(t) = x(t) \star h(t) + n(t). \quad (1)$$

where: $\star$ was the convolution operator, $y(t)$ the measured signal, $x(t)$ the reflectivity function, $h(t)$ the system impulse response and $n(t)$ is a Gaussian white noise.
If we applied the logarithm to the left and right members of the spectrum signal presented in Eq. 1 we obtain the Cepstrum coefficients:

$$\log(Y(\omega)) = \log(H(\omega)) + \log(X(\omega)) \quad (2)$$

where log was the natural logarithm. The noise parameter is removed in Eq. 2 for computation simplicity.
Then we transformed the input signal in a linear operation. This could discriminate between the signals using the above presented suppositions that PSF was a much smooth function and the wave separation problem can be changed in a denoising one. The used algorithm was proposed in [5, 7]. The main idea of this technique was the use of a denoising method in the frequency domain by applying a wavelet soft thresholding and an outlier resistant denoising algorithm. For decomposition, we use a Daubechies function base and the level of decomposition was $J = 5$. The soft threshold was calculated using the formula $T = \sigma\sqrt{2\log(N)}$ where the σ is the noise standard deviation and N is the length of the signal. The σ parameter was estimated from the original signal using the formula [20]:

$$\sigma = \frac{M_x}{0.6745}. \quad (3)$$

where M_x was the median absolute value of the finest decomposition level.
The second step was the execution of the deconvolution method. For this level we implemented a 1D version of the CLEAN algorithm:

1. we started with a copy of original signal which was called Dirty wave and found the highest point of them;
2. A blank wave, representing the Cleaned wave was set with the same length of Dirty wave and all positions equals to zero;
3. The normalised PSF, was multiplied with the value of the maximum point from Dirty wave and a parameter γ named "loop gain";
4. The resulting PSF was translated with the maximum point position in the maximum *Dirty wave* position and was subtracted from it;
5. We reexamined the residual wave to find the newest brightest pixel.

The points of subtracting the PSF multiplied by the maxima of the signal (steps 3, 4, 5) were repeated until an exit criteria is accomplished. This criteria was usually a constant threshold and the iterative loop was executed until the residual signal is lower then it.
For this algorithm we use the RF signal envelope from two reasons. Firstly, it was easier to extract the PSF envelope without phase recovery, and secondly, the CLEAN algorithm worked only if the dirty wave was a positive function.

3 Simulations description

For the simulations we use sparse synthetic signals contaminated with the Gaussian white noise. The length of the signals is 512 points the sampling frequency is 20 MHz and the central transducer frequency is 3.2 MHz. This corresponds to sequence of 160 μs and a approximately 25 cm deep scanning (for a standard ultrasound velocity c = 1540 m/s).
The purpose of the simulations was to make a statistical point of view about the proposed deconvolution method in the ultrasound domain. We had two important directions of study in function of the next questions: "How the proposed method work in functions of different SNR values?" and "How the method work in function of sparsity density of the reflectivity function?". Following these questions we made two simulations presented step-by-step in the follows.
Simulation 1:

1. get a sparse signal with a fixed density f;
2. for each SNR value
3. for each trial we made: $f = f + noise(SNR)$, the convolution between f and an ideal PSF, the PSF estimation using the homomorphic deconvolution;
4. for each threshold value make the CLEAN deconvolution and find the number of the true and false peaks resulted;
5. go to 3. until all number of trials was executed;
6. go to 2. until all SNR values was tested;
7. Results statistical evaluation.

The trials was proposed to generate different noise distributions for the same SNR which ensured us that the evaluated signal had different aspects and the obtained result was not an exception. The "loop gain" γ for the CLEAN was set to 1. We chose this value because we wanted to make a fast algorithm, and the experimental results showed that it had not a substantial improvement in the final cleaned signal.
Simulation 2: The second experiment was oriented to study of the proposed method in the case when the tissues reflectivity function is more dense. We executed the above presented algorithm with some modifications. In this case the SNR was fixed to a value and the sparse density of the signal was modified.
The evaluation criteria for the algorithm was oriented to verify how much of the resulted "Clean wave" had a real signal and how much not. That means we count after every execution of the CLEAN method the number of the peaks which can be considered real or not. We realized a detector which used a spatial window, with a predefined size. We centred the window on each original peak position and looked in the resulted signal if we had or not peaks in it. At the end we counted the total number of matched positions, which was the number or real peaks and, total number of false peaks. The total number of real peaks was divided by the number of real peaks, for better reading accuracy. Tolerance window was set to be a little value. For our signal of 512 samples length the selected tolerance was 1% from the length. In term of the ultrasound parameters this represented approximately 2,4 mm position error precision.

4 Results and discussions

The results and discussions were focused on the proposed experiments and were divided in two categories: the influence of the noise in the deconvolution algorithm and the influence of peaks density in signal recovery.

Simulation 1: In the Figure 1 we presented the simulations results according to different types of SNR. For this simulations we tested the reflectivity function signals with SNR equal to 5, 10, 15 and 20 dB. In the top was displayed the peak detection number percentage which represent the number of the true peaks found for different threshold values, and in bottom the number of the false alarms according to the threshold values. We can see that the number of real peaks recovered by the algorithm was linear dependent and inverse proportionally with the threshold. This result was caused by the function reflectivity density, whose peaks were not with the same amplitude. For a 10% level the number of the real peaks was approximately 75-80% which could be considered a good value. The real problems started when the threshold reach the noise level. We could see that the number of the false alarms increase exponentially, and offered incorrect informations about the scanned tissues. The false alarms was also, dependent on the SNR value. From the simulations we could say that the SNR value has a directly proportional influence for the false alarms detection.

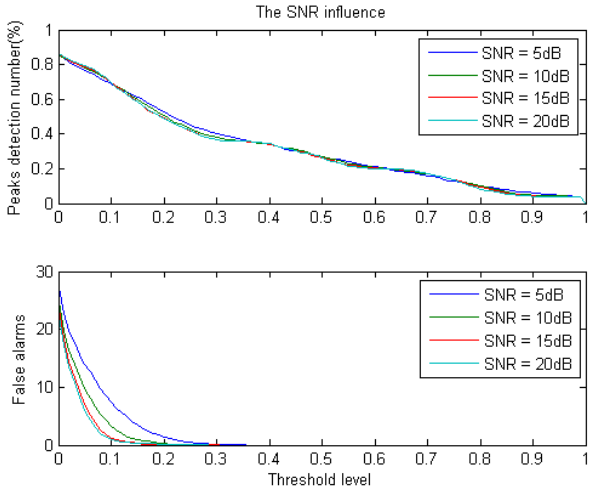

Figure 1: The results simulations with different types of SNR. Top: the peak detection number percentage (%) in function of the threshold value; bottom: the number of false peaks.

Simulation 2: The second experiment was focused to evaluate the performances of this method in function of the number of peaks which constitute the original sparse signal. In the Figure 2 we presented the result obtained for sparse signals with 1, 5 and 10% sparse density. The added noise was simulated to guarantee a SNR value equal to 15dB. In the upper graph we showed the percentage of the real extracted peaks according to the sparsity density, *i.e.* the number of the peaks higher then 0 in the original generated signal. One saw that the sparsity density influence the detection probability. For example, for a signal with 1% density factor the algorithm worked in good conditions. For a level of threshold equals to 10% it recovered up then 90% from the original peaks and has a low level of false alarms, but for a signal with 10% the percentage was between 50% and 60% for the same threshold.

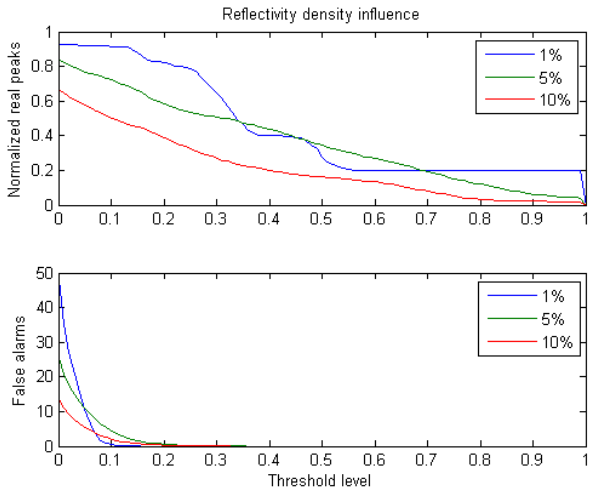

Figure 2: The results simulations with different types of peaks density. Top: the peak detection number percentage (%) in function of the threshold value; bottom: the number of false peaks.

Therefore, for the sparse signals with a low density the proposed algorithm worked well, but for the high densities the algorithm performance suffered. In the bottom graph of the Figure 2 is displayed the number of the false detected peaks, which appeared to not be conclusive for this experiment.The algorithm worked well in scanned mediums with few reflectivity points and had a low sensitivity to the noise.

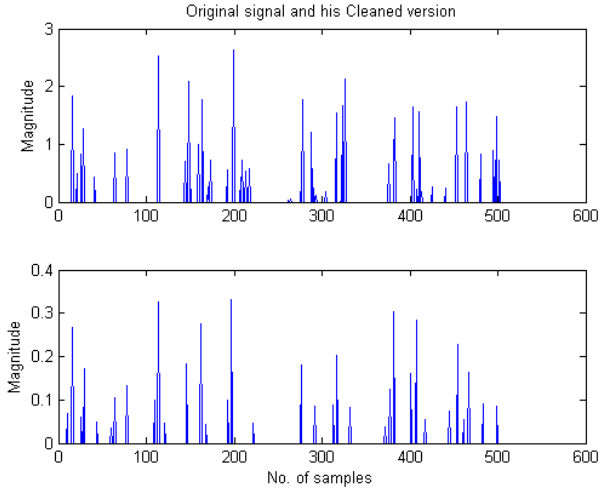

Figure 3: The final result for the algorithm. Top: the original sparse signal; bottom: The resulted Clean version.

The real problems appeared when the density increase. From our simulations, this problem had one great cause. It was the problem of the CLEAN algorithm, which was not able to discriminate 2 peaks when the Rayleigh criterion was not accomplished ($\lambda_{PSF}/2 < d$, where λ_{PSF} was the wavelength of the estimated PSF and, d was the distance between two peaks).

In the Figure 3 we showed the resulted Cleaned version of the extracted from the RF signal with the Clean method. The signal had a density equals with 10% from the length of the signal and a threshold equals to 0.1 from maximum of the envelope. The threshold was selected manually using an mod-

ified ROC curve where the x axis was the number of false alarms and the y axis was the normalised number of the real detected peaks. The final amplification was not our purpose, and for that, we presented the Cleaned version without amplification factor. The obtained signal appeared to well working when the peaks was sparse but when there were more dense the algorithm was not capable to discriminate all of them.

5 Conclusion

The proposed Blind CLEAN deconvolution was a method which work well when we had a little number of the scatters in the scanned tissues and it had the capability to improve the image contrast. Also, it appeared to be able to detect the peaks until the noise level without trouble. The problems appeared when the signal is more dense. Then the method was incapable to extract all the peaks, *i.e.* the proposed method was incapable to increase the resolution. From the presented tests we showed that we can go until the Rayleigh criterion.

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